RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/620256

Source: IFW

Date Processed by STIC: 12/3/4

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IFWO

RAW SEQUENCE LISTING   DATE: 12/03/2004
PATENT APPLICATION: US/10/620,256   TIME: 12:32:51

Input Set : N:\Crf3\RULE60\10620256.raw
Output Set: N:\CRF4\12032004\J620256.raw

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 1 <110> APPLICANT: Conneely, Orla M
 2        Headon, Denis R.
 3        O'Malley, Bert W.
 4        May, Gregory S.
 5 <120> TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
 6        AND LACTOFERRIN POLYPEPTIDES USING cDNA SEQUENCES IN VARIOUS
 7        ORGANISMS
 8 <130> FILE REFERENCE: 01380023US02
 9 <140> CURRENT APPLICATION NUMBER: US/10/620,256
10 <141> CURRENT FILING DATE: 2003-07-15
11 <150> PRIOR APPLICATION NUMBER: US/09/633,739
12 <151> PRIOR FILING DATE: 2000-08-07
13 <150> PRIOR APPLICATION NUMBER: 08/456,108
14 <151> PRIOR FILING DATE: 1995-05-30
15 <160> NUMBER OF SEQ ID NOS: 14
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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19 <211> LENGTH: 2360
20 <212> TYPE: DNA
21 <213> ORGANISM: Homo sapiens
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25        aggccacaaa atgcttccaa tggcaaagga atatgagaag agtgcgtggc cctcctgtca     180
26        gctgcataaa gagagactcc cccatccagt gtatccaggc cattgcggaa aacagggccg     240
27        atgctgtgac ccttgatggt ggtttcatat acgaggcagg cctggccccc tacaaactgc     300
28        gacctgtagc ggcggaagtc tacgggaccg aaagacagcc acgaactcac tattatgccg     360
29        tggctgtggt gaagaagggc ggcagctttc agctgaacga actgcaaggt ctgaagtcct     420
30        gccacacagg ccttcgcagg accgctggat ggaatgtgcc tataggggaca cttcgtccat     480
31        tcttgaattg gacgggtcca cctgagccca ttgaggcagc tgtggccagg ttcttctcag     540
32        ccagctgtgt tcccggtgca gataaaggac agttccccaa cctgtgtcgc ctgtgtgcgg     600
33        ggacagggga aaacaaatgt gccttctcct cccaggaacc gtacttcagc tactctggtg     660
34        ccttcaagtg tctgagagac ggggctggag acgtggcttt tatcagagag agcacagtgt     720
35        ttgaggacct gtcagacgag gctgaaaggg acgagtatga gttactctgc ccagacaaca     780
36        ctcggaagcc agtggacaag ttcaaagact gccatctggc ccgggtccct tctcatgccg     840
37        ttgtggcacg aagtgtgaat ggcaaggagg atgccatctg gaatcttctc cgccaggcac     900
38        aggaaaagtt tggaaaggac aagtcaccga aattccagct ctttggctcc cctagtgggc     960
39        agaaagatct gctgttcaag gactctgcca ttgggttttc gagggtgccc ccgaggatag    1020
40        attctgggct gtaccttggc tccggctact tcactgccat ccagaacttg aggaaaagtg    1080
41        aggaggaagt ggctgcccgg cgtgcgcggg tcgtgtggtg tgcggtgggc gagcaggagc    1140
42        tgcgcaagtg taaccagtgg agtggcttga gcgaaggcag cgtgacctgc tcctcggcct    1200
43        ccaccacaga ggactgcatc gccctggtgc tgaaaggaga agctgatgcc atgagtttgg    1260
44        atggaggata tgtgtacact gcaggcaaat gtggtttggt gcctgtcctg gcagagaact    1320
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47        gcaagaagtc ctgccacacc gccgtggaca ggactgcagg ctggaatatc cccatgggcc    1500
48        tgctcttcaa ccagacgggc tcctgcaaat ttgatgaata tttcagtcaa agctgtgccc    1560
49        ctgggtctga cccgagatct aatctctgtg ctctgtgtat tggcgacgag cagggtgaga    1620
50        ataagtgcgt gcccaacagc aatgagagat actacggcta cactggggct ttccggtgcc    1680
51        tggctgagaa tgctggagac gttgcatttg tgaaagatgt cactgtcttg cagaacactg    1740
52        atggaaataa caatgaggca tgggctaagg atttgaagct ggcagacttt gcgctgctgt    1800
53        gcctcgatgg caaacggaag cctgtgactg aggctagaag ctgccatctt gccatggccc    1860
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55        accaacaggc taaatttggg agaaatggat ctgactgccc ggacaagttt tgcttattcc    1980
56        agtctgaaac caaaaacctt ctgttcaatg acaacactga gtgtctggcc agactccatg    2040
57        gcaaaacaac atatgaaaaa tatttgggac cacagtatgt cgcaggcatt actaatctga    2100
58        aaaagtgctc aacctccccc ctcctggaag cctgtgaatt cctcaggaag taaaaccgaa    2160
59        gaagatggcc cagctcccca agaaagcctc agccattcac tgcccccagc tcttctcccc    2220
60        aggtgtgttg gggccttggc tcccctgctg aaggtgggga ttgcccatcc atctgcttac    2280
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66  <212> TYPE: PRT
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72                     20                  25                  30
73        Gln Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Arg
74                 35                  40                  45
75        Val Arg Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln
76             50                  55                  60
77        Cys Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp
78         65                  70                  75                  80
79        Gly Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro
80                         85                  90                  95
81        Val Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr
82                    100                 105                 110
83        Tyr Ala Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu
84                    115                 120                 125
85        Leu Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly
86                130                 135                 140
87        Trp Asn Val Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly
88        145                 150                 155                 160
89        Pro Pro Glu Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser
90                        165                 170                 175
91        Cys Val Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu
92                    180                 185                 190
93        Cys Ala Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro
94                    195                 200                 205
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 96            210             215                 220
 97        Asp Val Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp
 98        225             230                 235                 240
 99        Glu Ala Glu Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg
100                        245                 250                 255
101         Lys Pro Val Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser
102                        260                 265                 270
103         His Ala Val Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp
104                        275                 280                 285
105         Asn Leu Leu Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro
106                        290                 295                 300
107         Lys Phe Gln Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe
108        305                 310                 315                 320
109         Lys Asp Ser Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser
110                        325                 330                 335
111         Gly Leu Tyr Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg
112                        340                 345                 350
113         Lys Ser Glu Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys
114                        355                 360                 365
115         Ala Val Gly Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu
116                        370                 375                 380
117         Ser Glu Gly Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys
118        385                 390                 395                 400
119         Ile Ala Leu Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly
120                        405                 410                 415
121         Gly Tyr Val Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala
122                        420                 425                 430
123         Glu Asn Tyr Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val
124                        435                 440                 445
125         Asp Arg Pro Val Glu Gly Tyr Leu Ala Val Ala Val Arg Arg Ser
126        450                 455                 460
127         Asp Thr Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His
128        465                 470                 475                 480
129         Thr Ala Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu
130                        485                 490                 495
131         Phe Asn Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser
132                        500                 505                 510
133         Cys Ala Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile
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135         Gly Asp Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg
136                        530                 535                 540
137         Tyr Tyr Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly
138        545                 550                 555                 560
139         Asp Val Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly
140                        565                 570                 575
141         Asn Asn Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala
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143         Leu Leu Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser
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144                595                    600                    605
145        Cys His Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp
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148        625                    630                    635                    640
149        Gly Arg Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser
150                    645                    650                    655
151        Glu Thr Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg
152                    660                    665                    670
153        Leu His Gly Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val
154                675                    680                    685
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161 <211> LENGTH: 2347
162 <212> TYPE: DNA
163 <213> ORGANISM: Bos taurus
164 <400> SEQUENCE: 3
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167        taccatctcc caacctgagt ggttcaaatg ccgcagatgg cagtggagga tgaagaagct     180
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171        aacccactat tatgctgtgg ccgtcgtgaa gaagggcagc aactttcagc tggaccagct     420
172        gcaaggccgg aagtcctgcc atacgggcct tggcaggtcc gctgggtgga tcatccctat     480
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176        cttcggttat tctggtgcct tcaagtgtct gcaggacggg gctggagacg tggctttttgt     720
177        taaagagacg acagtgtttg agaacttgcc agagaaggct gacagggacc agtatgagct     780
178        tctctgcctg aacaacagtc gggcgccagt ggatgcgttc aaggagtgcc acctggccca     840
179        ggtcccttct catgctgtcg tggcccgaag tgtggatggc aaggaagact tgatctggaa     900
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182        gatcccctcg aaggtagatt cggcgctgta cctgggctcc cgctacttga ccaccttgaa    1080
183        gaacctcagg gaaactgcgg aggaggtgaa ggcgcggtac accagggtcg tgtggtgtgc    1140
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188        aacggaaggg taccttgccg tggcagttgt caagaaagca aatgaggggc tcacatggaa    1440
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198      ttgtttgttc aaatctgaaa ccaaaaacct tctgttcaat gacaacactg agtgtctggc   2040
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200      tgccaacctg aaaaaatgct caacctcccc gcttctggaa gcctgcgcct tcctgacgag   2160
201      gtaaagcctg caaagaagct agcctgcctc cctgggcctc agctcctccc tgctctcagc   2220
202      cccaatctcc aggcgcgagg gaccttcctc tcccttcctg aagtcggatt tttgccaagc   2280
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206 <210> SEQ ID NO: 4
207 <211> LENGTH: 708
208 <212> TYPE: PRT
209 <213> ORGANISM: Bos taurus
210 <400> SEQUENCE: 4

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214                   20                  25                  30
215      Pro Glu Trp Phe Lys Cys Arg Arg Trp Gln Trp Arg Met Lys Lys Leu
216                   35                  40                  45
217      Gly Ala Pro Ser Ile Thr Cys Val Arg Arg Ala Phe Ala Leu Glu Cys
218           50                  55                  60
219      Ile Pro Gly Ile Ala Glu Lys Lys Ala Asp Ala Val Thr Leu Asp Gly
220      65                  70                  75                  80
221      Gly Met Val Phe Glu Ala Gly Arg Asp Pro Tyr Lys Leu Arg Pro Val
222                   85                  90                  95
223      Ala Ala Glu Ile Tyr Gly Thr Lys Glu Ser Pro Gln Thr His Tyr Tyr
224                   100                 105                 110
225      Ala Val Ala Val Val Lys Lys Gly Ser Asn Phe Gln Leu Asp Gln Leu
226                   115                 120                 125
227      Gln Gly Arg Lys Ser Cys His Thr Gly Leu Gly Arg Ser Ala Gly Trp
228           130                 135                 140
229      Ile Ile Pro Met Gly Ile Leu Arg Pro Tyr Leu Ser Trp Thr Glu Ser
230      145                 150                 155                 160
231      Leu Glu Pro Leu Gln Gly Ala Val Ala Lys Phe Phe Ser Ala Ser Cys
232                   165                 170                 175
233      Val Pro Cys Ile Asp Arg Gln Ala Tyr Pro Asn Leu Cys Gln Leu Cys
234                   180                 185                 190
235      Lys Gly Glu Gly Glu Asn Gln Cys Ala Cys Ser Ser Arg Glu Pro Tyr
236                   195                 200                 205
237      Phe Gly Tyr Ser Gly Ala Phe Lys Cys Leu Gln Asp Gly Ala Gly Asp
238           210                 215                 220
239      Val Ala Phe Val Lys Glu Thr Thr Val Phe Glu Asn Leu Pro Glu Lys
240      225                 230                 235                 240
241      Ala Asp Arg Asp Gln Tyr Glu Leu Leu Cys Leu Asn Asn Ser Arg Ala
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243      Pro Val Asp Ala Phe Lys Glu Cys His Leu Ala Gln Val Pro Ser His
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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/620,256

DATE: 12/03/2004
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